

Ascorbic acid inhibition of *Candida albicans* Hsp90-mediated morphogenesis occurs via the transcriptional regulator Upc2.

Running title: Ascorbic acid affects elongation upon Hsp90 compromise

Frédérique Van Hauwenhuyse^{1,2}, Alessandro Fiori^{1,2}, Patrick Van Dijck^{1,2,#}

¹ Department of Molecular Microbiology, VIB, Leuven, Belgium

² Laboratory of Molecular Cell Biology, KU Leuven, Kasteelpark Arenberg 31 bus 2438, 3001 Leuven, Belgium

[#]To whom correspondence should be addressed

Patrick Van Dijck

Laboratory of Molecular Cell Biology, KU Leuven

Department for Molecular Microbiology, VIB

Kasteelpark Arenberg 31 bus 2438

3001 Heverlee, Belgium

Tel.: (0032) 16 321512

Fax: (0032) 16 321979

E-mail: Patrick.vandijck@mmbio.vib-kuleuven.be

Abstract

Morphogenetic transitions of the opportunistic fungal pathogen *Candida albicans* are influenced by temperature changes, with induction of filamentation upon a shift from 30 to 37°C. Hsp90 was identified as a major repressor of an elongated cell shape morphology at low temperatures, as treatment with specific inhibitors of Hsp90 results in elongated growth forms at 30°C. Elongated growth resulting from a compromised Hsp90 is considered neither hyphal nor pseudohyphal growth. It has already been reported that ascorbic acid (Vitamin C) interferes with the yeast-to-hyphae transition in *C. albicans*. In the present study, we show that ascorbic acid also antagonizes the morphogenetic change caused by hampered Hsp90 function. Further analysis revealed that Upc2, a transcriptional regulator of genes involved in ergosterol biosynthesis, and Erg11, the target of azole antifungals whose expression is in turn regulated by Upc2, are required for this antagonism. Ergosterol levels correlate with elongated growth, being reduced in cells treated with the Hsp90 inhibitor Geldanamycin (GdA), and restored by co-treatment with ascorbic acid.

In addition, we illustrate that Upc2 appears to be required for ascorbic acid-mediated inhibition of the antifungal activity of fluconazole. These results identify Upc2 as a major regulator of ascorbic acid-induced effects in *C. albicans* and suggest an association between ergosterol content and elongated growth upon Hsp90 compromise.

Introduction

Candida albicans belongs to the few fungal species that are frequently encountered as clinical pathogens (1). *C. albicans* is a frequent commensal of healthy individuals but when the host immune system is weakened, it can become a deadly pathogen (2). Its pathogenic nature relies on a multitude of factors, including the ability to grow at 37 °C, to produce adhesins and hydrolases and to change between different morphological forms, including yeast cells, hyphae, pseudohyphae, chlamydospores, opaque cells and the recently described GUT morphology (3-5). It is generally assumed that the yeast form is crucial for fungal dissemination via the bloodstream throughout the body (6), while hyphae on the other hand are required for the production of extracellular enzymes and invasive growth (7).

The yeast-to-hyphae transition of *C. albicans* can be triggered by environmental cues such as pH, serum, elevated temperature and CO₂ (4, 8). In addition several small molecules, such as autoregulatory molecules, cell cycle inhibitors and histone deacetylase inhibitors, are also capable of modulating morphogenetic responses (9, 10). Most environmental triggers and small molecules function through activation of the cAMP-PKA or MAPK pathways via their downstream transcription factors Efg1 and Cph1, respectively (4, 11, 12). Over the past few years, several reports appeared that showed that Geldanamycin (GdA), a benzoquinone ansamycin antibiotic is another small molecule that strongly affects the cell shape of *C. albicans* at 30 °C as its addition results in elongated cells. GdA inhibits the function of Hsp90 by binding to its ADP/ATP binding pocket (10, 13) indicating that Hsp90 prevents an elongated cell shape of *C. albicans* at lower temperatures. This morphogenetic process also involves the Ras1-

cAMP-PKA signalling pathway but it seems to do this independent of the downstream transcription factor Efg1, suggesting the involvement of other transcriptional regulators (13). Screening of a transcription factor (TF) deletion collection for mutants impaired in the Hsp90-mediated elongated cell shape phenotype, resulted in the identification of Hms1 (14). Two upstream regulators of this TF, the cyclin-dependent kinase Pho85 and the cyclin Pcl1 are also required for elongated cell shape (14). As Hms1 is not a component of the cAMP-PKA pathway, the link between Hsp90-dependent elongated cell shape and the Ras1-PKA signalling pathway remained to be identified. Our aim in this work was to identify transcription factors that upon overexpression affect the Hsp90-dependent elongated cell shape. For this we screened a TF overexpression library and we found that overexpression of Upc2 prevents the elongated growth phenotype when GdA is added. The Zn₂Cys₆ transcriptional regulator Upc2 is important for the regulation of the ergosterol biosynthetic pathway in response to commonly used antifungals (15). This transcription factor can act as a repressor or an activator depending on its target and on the initiating conditions, and exerts its function by binding to sterol response elements (SREs) (15-17). Gain-of-function mutations in *UPC2* have been associated with resistance to antifungal treatments (18-21), while strains devoid of Upc2 are hypersusceptible to azole antifungals (22). One of the genes regulated by Upc2 is Erg11, which is a key enzyme in the biosynthesis of ergosterol and it is the target of the azole antifungal drugs. Overexpression of Erg11 has been shown to cause tolerance to these drugs.

In order to find components linking the GdA-induced elongated growth phenotype and the block of this phenotype upon overexpression of *UPC2*, we have tested a number of

compounds that were shown to mediate morphogenesis in *C. albicans*. Ascorbic acid (vitamin C) was previously shown to play a role in morphogenesis as it blocks serum-initiated hyphae formation, a process mediated by adenylate cyclase (23, 24). How ascorbic acid affects morphogenesis is not clear and we propose that it may function by modulating the role of Hsp90 in cell shape formation. In this paper, we describe a previously unreported negative effect of ascorbic acid on the Hsp90-dependent cell shape. Focusing on the mode of action of ascorbic acid, we provide evidence that it requires Upc2 and Erg11 to exert its function. We further demonstrate that intracellular ergosterol levels play a role in the ascorbic acid mediated effect on cell shape. In addition, we show that Upc2 is also required for the antagonistic effect of ascorbic acid on fluconazole toxicity. Together, these results show that ascorbic acid inhibits the Hsp90-mediated cell shape transition via the transcriptional regulator Upc2.

Materials and methods

Strains and growth conditions

Strains used in this study are listed in Table 1. *C. albicans* strains were grown overnight in 3 ml of YPD (1 % yeast extract, 2 % bacteriological peptone and 2 % glucose) at 30°C. Cells were subsequently diluted to OD₆₀₀=0.2 and cultured for indicated time points at 30°C with the indicated treatment (4 µM or 10 µM Geldanamycin; 2.5 mM ascorbic acid, L-cysteine, D-cysteine, glutathione or dithiotreitol (DTT), 0.1 µg/ml doxycycline). When ascorbic acid was added, the medium was buffered to pH 7. All chemicals were purchased from Sigma-Aldrich.

Transcription factor overexpression strains were grown in Complete supplement mixture minus methionine (CSM-Met medium : 0.073 % CSM-Met-Ura, 0.17 % YNB w/o amino acids and $(\text{NH}_4)_2\text{SO}_4$, 0.5 % $(\text{NH}_4)_2\text{SO}_4$, pH5.5) supplemented with 0.1 % uridine and the indicated treatment (10 μM GdA, 2.5 or 10 mM methionine).

Microscopy

Imaging of the cells was done by differential interference contrast microscopy using the Zeiss Axioplan 2 microscope. Images were obtained by a Zeiss AxioCam MRc5 camera using Axiovision software 3.0 (Carl Zeiss, Inc. NY).

Cell sedimentation assay

The cell-sedimentation rate was quantified using the assay described by Eboigbodin and Biggs (25) and Fu *et al.* (26). Cells were grown in YPD liquid medium with (0.1 $\mu\text{g/ml}$, for transcriptional repression) or without doxycycline and 2.5 mM of L-cysteine or ascorbic acid. OD_{600} was determined at indicated time points of the cells at the upper part of the glass tube, as sediments settle to the bottom of the glass tube. The formula $(\text{OD}_i - \text{OD}_t / \text{OD}_i) \times 100$ was utilized to calculate the percentage of sedimented cells. OD_i is the initial OD taken at time zero and OD_t is the OD taken at the indicated time point.

Upc2 overexpression strain: Transcription factor library

The *UPC2* overexpression strain used in this study is part of a transcription factor overexpression library, constructed in our laboratory on the basis of the previously developed *Candida albicans* two-hybrid system (27). Briefly, the nuclear localization

sequence (NLS) was removed from the one-hybrid plasmid pC2HB resulting in pC1H. Subsequently, genes encoding known and putative transcription factors were successfully cloned in fusion with the DNA-binding domain LexA in this plasmid, to create the pC1H-PTF library. The resulting plasmids were integrated in the two-hybrid reporter strain S2CH3 (27) between *XOG1* and *HOL1* loci on chromosome 1 after linearization at the *NotI* restriction site. Selection was performed on CSM-leu medium. The complete library consists of ~200 strains, each carrying an ectopically expressed protein, under the control of an inducible *MET3* promoter (Stynen *et al.*, under preparation). The use of the inducible *MET3* promoter allows for a conditional expression, as it is repressed in the presence of methionine and cysteine (28).

Ergosterol extraction and quantification

Ergosterol extraction and quantification was performed as reported by Arthington-Skaggs *et al.* (29), with minor modifications. Briefly, cells were grown overnight in 4 ml YPD at 30 °C. Cells were diluted to OD₆₀₀=0.2 and grown in YPD medium supplemented with 10 µM GdA, 2.5 mM ascorbic acid or a combination of both. After the indicated time period, 220 ODs of cells at 600 nm [concentration of cells (OD/ml) x volume (ml) = 220 OD] were used in the heptane extraction. The same procedure was used for all experimental conditions. Cells were harvested by centrifugation at 3.000 rpm for 5 min and washed once with 10 ml sterile water. Three milliliters of 25 % alcoholic potassium hydroxide solution (25 g KOH and 35 ml sterile H₂O were brought to 100 ml with 100 % ethanol) was added to each pellet and vortexed for 1 minute. Cell suspensions were heated in an 85 °C water bath for 1 hour, then allowed to cool down at room temperature.

Sterols were extracted with a mixture of 1 ml of sterile water and 3 ml of n-heptane followed by mixing for 3 min. The organic layer was transferred to a clean glass tube and stored at -20°C for 24 h. Prior to the spectrophotometrical scan between 230 and 300 nm using a Shimadzu UV-1650PC spectrophotometer, sterol extracts were diluted fivefold in 100% ethanol. A dilution of heptane and ethanol was used as the blank. Ergosterol levels were subsequently calculated as a percentage of the wet weight as described (29).

Quantitative real-time PCR

Overnight cultures of *C. albicans* strains were diluted to an OD₆₀₀=0.2 and cultures were grown at 30 °C for the indicated time points in the presence and absence of either doxycycline (0.1 µg/ml), ascorbic acid (2.5 mM) and GdA (10 µM) before RNA extraction. RNA was DNase-treated prior to cDNA synthesis with the Promega A3500 reverse transcription kit. Quantitative real-time PCR was performed using the GoScript™ Reverse Transcription System (Promega) on a StepOne Plus real-time PCR system (Applied Biosystems). Reactions were performed in triplicate, with oligonucleotides CaERG11up, CaERG11down; Upc2_fw, Upc2_rv; Hsp90_fw, Hsp90_rv; TEF1a-fw and TEF1a-rv as the primer pairs (Table 2). The fold regulation was determined using the $\Delta\Delta C_t$ method, using expression of *TEF1* to normalize the data.

Checkerboard assay

A checkerboard assay on 96-well plates was performed, by combining different concentrations of ascorbic acid and fluconazole and the fractional inhibitory

concentration index (FICI) was determined. The assay was performed with both the wild type and the *UPC2* deletion mutant to verify whether the effect of ascorbic acid on fluconazole susceptibility is exerted via Upc2.

The concentrations of ascorbic acid ranged from 0.078 mM to 5 mM for both the wild type and the *UPC2* deletion mutant. The concentration of fluconazole ranged from 0.004 µg/ml to 2 µg/ml for the *UPC2* deletion mutant and 0.125 µg/ml to 64 µg/ml for the wild type. The FICI was calculated according to the formula $FIC_{index} = FIC_A + FIC_B = (MIC_{A \text{ comb}}/MIC_{A \text{ alone}}) + (MIC_{B \text{ comb}}/MIC_{B \text{ alone}})$, where $MIC_{A \text{ alone}}$ and $MIC_{B \text{ alone}}$ are the MICs of ascorbic acid and fluconazole alone and $MIC_{A \text{ comb}}$ and $MIC_{B \text{ comb}}$ are the MICs of ascorbic acid and fluconazole in combination. Interactions were referred to as synergistic when the FIC_{index} value was ≤ 0.5 and antagonistic when the FIC_{index} value was > 4 . FIC_{index} values that were > 0.5 and ≤ 4 indicated no interaction between ascorbic acid and fluconazole (30). There was no difference in FIC indexes observed between 24 and 48 h.

Oxidative stress sensitivity assay

The wild type and the two independent *UPC2* deletion mutants of the Homann collection (33) were grown to mid log phase in liquid YPD medium. Cells were diluted to OD_{600} of 1 and ten-fold serially dilutions were spotted on YPD plates containing the indicated concentrations of H_2O_2 . Plates were photographed after 24 hours incubation at 37°C.

Propidium iodide staining

Viability staining was performed by incubating a subset of cells (taken at the indicated time points of the experiments) for 20 min in the dark with the fluorescent stain

propidium iodide (PI; 46 mM) (Sigma-Aldrich). Prior to PI fluorescence analysis (excitation/emission maxima: 535/617 nm), cells were washed and resuspended in PBS.

Statistical analysis

Statistical significance was calculated using a student t-test analysis with ($P < 0.05 = *$) and ($P < 0.001 = **$). All experiments were performed with at least three biological repeats.

Results

Ascorbic acid interferes with the morphogenetic process governed by Hsp90

The transition from *C. albicans* yeast to hyphae can be induced or repressed by a wide variety of triggers (31). Partial inhibition of Hsp90, obtained by either addition of GdA, or by decreased transcription of the corresponding *HSP90* gene, results in elongated cells, which are considered neither hyphae nor pseudohyphae (13). In order to understand the mechanism by which Hsp90 affects morphogenesis, we have tested a number of compounds known to inhibit filamentation for interaction with GdA, and determined the effect of ascorbic acid on the GdA-induced elongated growth. Addition of ascorbic acid, which was previously reported to interfere with the yeast-to-hyphae transition (24), resulted in a strong reduction of the GdA-induced elongated cell shape (Figure 1A). Similar results were obtained using Radicicol, an Hsp90 inhibitor structurally distinct from GdA (32) (data not shown). Since Hsp90 is an essential chaperone, cell viability was assessed by propidium iodide (PI), a dye that is excluded from viable cells. As shown

in Figure 1B, the viability of GdA-treated cells is similar to that of untreated cells, ruling out possible effects due to elevated cell mortality.

To test whether the observed effect of ascorbic acid was dependent on Hsp90, or the result of chemical-chemical interference with GdA, similar experiments were conducted using a strain whose Hsp90 content can be modulated via the use of a tetracycline-repressible promoter (13). As expected, lowering the expression of *HSP90* with doxycycline in this strain resulted in elongated growth (Figure 2A). Cell viability was also tested here and indicated that cells were alive (Figure 2B). Addition of ascorbic acid to cells genetically depleted of Hsp90 greatly increased the percentage of yeast cells (75 %), as compared to the control condition without the addition of ascorbic acid (32 %) (Figure 2C). The effect of ascorbic acid was also determined using a sedimentation assay.

Addition of ascorbic acid to cells in a liquid culture resulted in a slower sedimentation rate, indicating a higher proportion of yeast cells in these cultures as compared to ascorbic acid-untreated cells (Figure 2D). Since transcription of *HSP90* in the *tetO-HSP90* strain is reduced in the presence of doxycycline, the possibility of a chemical doxycycline-ascorbic acid interaction was ruled out in experiments with wild type control cells. Here, the concentration of doxycycline used in our experiments was demonstrated to not interfere with the effect of ascorbic acid on the GdA-dependent elongated cell shape described above (Supplementary Figure 1A). We also confirmed that doxycycline-mediated repression of Hsp90 was not significantly altered in the presence of ascorbic acid (Supplementary Figure 1B). Taken together, these results indicate that ascorbic acid has a negative effect on elongated cell shape formation resulting from lower Hsp90 activity or expression.

Upc2 is required for the ascorbic acid-mediated effect.

A transcription factor deletion collection was previously used to characterize the regulatory system mediating Hsp90-regulated elongated growth (14). In a complementary approach, we have screened a transcription factor overexpression library to identify TFs that upon overexpression prevent GdA-induced morphogenesis. The library consists of ~200 strains, each carrying an ectopically expressed TF, under the control of the inducible *MET3* promoter (Stynen *et al.*, under preparation). Methionine only was used to repress transcription, as cysteine was shown to interfere with elongation even in a wild type strain due to its antioxidant properties (see discussion and Supplementary Figure 2). Several transcriptional regulators whose overexpression resulted in blocked or decreased elongated growth in the presence of GdA were identified (Table 3). We continued with the strain overexpressing *UPC2* (Figure 3A), as it showed the strongest effect, based on semi-quantitative observations. Expression of *UPC2* in inducing conditions was ~4.5-fold higher than an isogenic control strain carrying an empty plasmid (Figure 3A). As expected, the characteristic elongated growth form was visible when the *MET3* promoter was repressed by the addition of methionine, confirming that increased dosage of Upc2 is responsible for the loss of elongation in the presence of inactive Hsp90 (Figure 3B). To confirm the role of Upc2 in the Hsp90-mediated inhibition of elongated growth forms, we tested two independent strains in which the endogenous *UPC2* genes were deleted (22, 33), as such strains are expected to be hypersusceptible to GdA. Treatment of the wild type strain with low concentrations of GdA (4 μ M) has no effect on morphogenesis of wild type cells. However, the same concentration was sufficient to induce elongated

growth in the *upc2Δ/upc2Δ* strains, confirming their hypersusceptibility (strain D-6 is shown in Figure 4A). In the complemented strain, elongation was impaired (Figure 4A). Taken together, these observations indicate that Upc2 plays a role in the GdA-associated elongation process, and confirm the previously observed genetic interaction between Upc2 and Hsp90 (34).

The obvious question was then whether Upc2 is required for the effect that ascorbic acid has on the Hsp90-mediated cell elongation. Addition of ascorbic acid to wild type cells prevents the GdA-induced cell elongation. In the absence of Upc2 (in both independent deletion strains D-6 and TF077) the GdA-induced cell elongation was not affected whereas the *UPC2*-reconstituted strain EC-7 resulted in a similar phenotype as the wild type strain (Figure 4B). These results indicate that the effect of ascorbic acid on the morphological response upon inhibition of Hsp90 is Upc2-dependent.

Hsp90 inhibition or depletion results in reduced intracellular ergosterol levels

To determine the mechanism by which ascorbic acid and Upc2 affect elongated cell growth, we tested the role of genes whose expression are regulated by Upc2, such as the drug efflux pumps *CDR1* and *MDR1* (17, 35). First, we hypothesized that ascorbic acid could increase the efflux of GdA, which was reported to be a substrate of the human ABC (ATP-binding cassette) transporter efflux pump, Mdr1 (36, 37). If this hypothesis were valid in *C. albicans*, one would expect mutants lacking Cdr1, a fungal ABC multidrug transporter (38) to elongate in the presence of both GdA and ascorbic acid. In addition, one would expect a strain devoid of this efflux pump to be hypersusceptible to GdA.

296 However, neither hypersusceptibility to GdA nor impairment of the morphogenetic effect
297 of ascorbic acid was observed for the *cdr1Δ/cdr1Δ* mutant (data not shown).

298 We also investigated Mdr1, a member of the multidrug resistance (MDR1) major
299 facilitator family. Strains overexpressing *MDR1* (39) or deleted for *MDR1* were not
300 affected in the ascorbic acid-mediated effect and were not hypersusceptible to GdA (data
301 not shown). Together, these results rule out the hypothesis that an ascorbic acid-mediated
302 increased efflux of GdA is causative for the ascorbic acid-mediated phenotype.

303 Apart from *CDR1* and *MDR1*, expression of *ERG11*, a key gene in the ergosterol
304 biosynthesis pathway, is also under the control of Upc2 (15, 22, 40). We therefore
305 reasoned that levels of Erg11 might play an instrumental role in the morphogenetic
306 transition regulated by Hsp90. The role of Erg11 on the ascorbic acid induced inhibition
307 was investigated using an engineered strain in which the only *ERG11* allele is under the
308 control of a tetracycline-repressible promoter (41). Cells, in which the transcription of
309 *ERG11* was repressed by the addition of doxycyclin, but that were still viable
310 (Supplementary Figure 3), were tested for GdA-induced elongation in the presence of
311 ascorbic acid. As shown in Figure 5A (compare a, c, g and h), Erg11 expression is
312 required for the ascorbic acid induced inhibition of cell elongation upon GdA treatment.

313 We also tested an *ERG11* overexpression strain (~3.5-fold higher expression compared to
314 the control strain) (42) but, as shown in Figure 5B, such increased dosage of *ERG11* was
315 not able to suppress the elongated phenotype upon Hsp90 inhibition, demonstrating that
316 an increased dosage of Erg11 is not sufficient to block GdA-induced elongation. We also
317 investigated whether ascorbic acid induces *ERG11* expression in the presence and
318 absence of Hsp90 inhibitors. In the wild type strain, there is a significant drop in *ERG11*

expression upon GdA treatment, while simultaneous addition of ascorbic acid upon this treatment leads to an increased transcription of *ERG11* (Figure 5C). This increase is absent in an *upc2Δ/upc2Δ* mutant, suggesting a role for Upc2 as an important regulator. Erg11's eminent role in the regulation of sterol biosynthesis (15, 22, 43) and ascorbic acid-mediated effects on the Hsp90 morphogenetic circuitry (Figure 1A and 2A), suggests a possible relationship between ergosterol content and ascorbic acid induced inhibition of cell elongation in the presence of GdA. To verify the impact of an impaired Hsp90 function on ergosterol levels, we determined ergosterol levels in wild type and *upc2Δ/upc2Δ* strains upon treatment with GdA (10 μM) and/or ascorbic acid (2.5 mM). As shown in Figure 6A, a significant decrease in ergosterol levels can be observed after addition of GdA to the wild type strain ($P < 0.05$) and the *upc2Δ/upc2Δ* mutant ($P < 0.001$) compared to the corresponding untreated control strains. Whereas ergosterol levels are restored when ascorbic acid (2.5 mM) is added together with GdA to the wild type strain, addition of both compounds to *upc2Δ/upc2Δ* cells failed to show a similar restoration. The difference in ergosterol levels compared to the untreated *upc2Δ/upc2Δ* mutant remained significant ($P < 0.05$). As can be seen, there is also a detectable decrease in ergosterol levels when ascorbic acid alone is administered, but this reduction is not significant ($P > 0.05$). These results point to a correlation between ergosterol levels and Hsp90-governed elongated growth. To rule that reduced ergosterol levels were the result of oxidative stress caused by the absence of Upc2 as was previously claimed (44), we tested the two independent *upc2* mutant strains from the Homann collection (33) that we used throughout our paper, for their susceptibility towards oxidative stress. Supplementary figure 4 shows that the tolerance to H₂O₂ of the mutants is absolutely

comparable to that of the corresponding isogenic wild type strain, thus ruling out the hypothesis that deletion of *UPC2* could lower the anti oxidative stress potential of the cells. Different response of other *upc2* mutants to oxidative stress may have different causes, such as a different genetic background (44).

Results obtained with pharmacological inhibition of Hsp90 were confirmed using genetic depletion of Hsp90. The *tetO-HSP90/hsp90Δ* strain was grown in the presence and absence of doxycycline and ergosterol levels were determined. As shown in Figure 6B, depletion of Hsp90 results in a significant decrease in ergosterol levels ($P < 0.001$). Similar to the pharmacological inhibition, addition of ascorbic acid results in restoration of ergosterol levels, with higher ergosterol in the presence of higher ascorbic acid. To rule out a more indirect effect of ascorbic acid on ergosterol levels via its antioxidant effect we have analyzed ROS production by way of rhodamine fluorescence in the wild type strain and in the *Tet0-HSP90/hsp90Δ* strain in the presence or absence of doxycycline, and with or without ascorbic acid. Fluorescence of doxycycline-, as well as of doxycycline and ascorbic acid-treated cells was comparable to that of untreated cells. H₂O₂-treated cells were used as the positive control (data not shown).

These results suggest that decreased ergosterol levels caused by Hsp90 inhibition (Figure 6A and 6B) promote elongated growth. However, Figure 5A (panel d) shows that a reduction of ergosterol levels (by downregulating *ERG11* expression) was not sufficient to induce elongation, since elongated growth forms still required Hsp90 inhibition.

To our knowledge, this is the first time that a clear correlation between impaired/decreased Hsp90 expression, and ergosterol levels has been observed.

Moreover, addition of ascorbic acid restores ergosterol levels to wild type levels and this is clearer upon pharmacological inhibition, compared to genetic depletion of Hsp90.

Upc2 is required for other ascorbic acid-mediated effects

It has been reported in previous studies that ascorbic acid reduces the antifungal effect of fluconazole, possibly via its antioxidant properties (45). The authors suggested that the antioxidant properties of ascorbic acid counteract fluconazole-induced reactive oxygen species, resulting in a similar effect obtained with other antioxidants such as glutathione (45). In order to establish a general role for Upc2 in orchestrating ascorbic acid-mediated phenomena, we verified a possible relationship between ascorbic acid and fluconazole in a *upc2Δ/upc2Δ* strain by means of checkerboard assays, two-dimensional tests designed to measure drug-drug interactions. Fluconazole and ascorbic acid display antagonistic activity, as determined via the calculation of the fractional inhibitory concentration (FIC) index (FIC index 33, Table 4). This kind of interaction is no longer detectable when the checkerboard is performed using cells of the *upc2Δ/upc2Δ* strain (FIC index 0.75, Table 4). Thus, the combination of ascorbic acid with fluconazole no longer displayed antagonistic activity in cells lacking the Upc2 transcription factor.

Discussion

Decreased dosage of Hsp90, as well as its pharmacologic depletion, results in a morphology change of *C. albicans* at low temperature from yeast to elongated cells (13). The molecular mechanism of this morphogenetic transition has been studied extensively

387 over the last few years (46, 47). We contribute to this characterisation by showing that
388 reduced levels of ergosterol result from GdA-mediated impairment of Hsp90, and that
389 these changes correlate with elongated growth. The effect of GdA can be suppressed by
390 addition of ascorbic acid, as this again increased levels of ergosterol to normal and
391 resulted in cell growth in the yeast form. Ascorbic acid suppression did not depend on its
392 anti oxidant activity, but depends on the transcriptional regulator Upc2, as in a
393 *upc2Δ/upc2Δ* mutant ascorbic acid cannot restore ergosterol levels to normal upon GdA
394 treatment. In summary, ascorbic acid can block the GdA-dependent elongated growth by
395 restoring normal ergosterol levels in a Upc2-dependent fashion.

396 In the course of our work we found that several antioxidants interfered with the activity
397 of GdA. Apart from its known inhibition of Hsp90, GdA is also involved in the
398 generation of superoxide radicals, which is attributed to the presence of its quinone group
399 (48). The presence of molecules with antioxidant properties alleviates the detrimental
400 effects of oxidative stress imposed by free radicals. A variety of molecules such as
401 reduced glutathione (GSH) and its derivatives, cysteine, dithiothreitol and ascorbic acid
402 are able to fulfil these protective requirements (49). It could be possible that the
403 superoxide radicals produced in the presence of GdA could affect the elongated cell
404 shape formation and addition of ascorbic acid would then block this through its anti
405 oxidant activities. This would fit with data obtained by Patterson et al. (50) who showed
406 that H₂O₂-mediated activation of Cap1 was a prerequisite for yeast to hyphae transition.

407 However, the fact that the antagonistic effect of ascorbic acid on morphology is observed
408 on cells genetically depleted of Hsp90 as well as on cells whose Hsp90 is inhibited by
409 GdA, suggests that ascorbic acid acts directly or indirectly on Hsp90 or Hsp90-mediated

processes. Other authors have reported an influence of ascorbic acid or its analogues on morphogenetic transitions in *C. albicans* (23, 24, 51). Nasution and colleagues (23) reported that addition of ascorbic acid not only lowered the intracellular concentration of reactive oxygen species, but also inhibited H₂O₂ and serum-initiated hyphal differentiation. Ojha and co-workers (24) similarly demonstrated inhibition of serum-induced hyphal formation by ascorbic acid and suggested a mode of action by interruption of the hyphal formation signal of *C. albicans*.

During the TF overexpression screening, we observed that cysteine directly affected the activity of GdA as no elongated growth could be observed in the wild type strain. This could be explained by earlier reports describing that thiol-containing antioxidants (such as cysteine) could physically interact with Hsp90 inhibitors, such as GdA and Radicicol, and render them inactive as a consequence of the thiol-mediated interaction (52-57). This means that one has to be careful when using the *MET3*-promoter in combination with GdA or Radicicol as in this case cysteine, that is used to repress the promoter, will affect the activity of GdA and Radicicol. This is the reason why in our experiments we used only methionine to repress the *MET3* promoter.

One of the TFs that inhibited the GdA-induced morphogenesis was Upc2, a Zn₂Cys₆ transcription factor, a key regulator of drug efflux pump expression and ergosterol biosynthesis (15, 35). Here we show that Upc2 is required for the ascorbic acid inhibition of cell elongation upon compromised Hsp90 function. Previously it was already shown that Upc2 is a key regulator of the ascorbic acid-mediated effect on fluconazole, as it decreases the antifungal effect of fluconazole, so displaying a protective role in fungi

(45). Together, these data show that Upc2 plays a central role as the transcriptional regulator in ascorbic acid-associated phenomena. Ascorbic acid is very important for human life because of its antioxidant properties, protecting cells from oxidative stress (58). The use of ascorbic acid is even clinically relevant for the treatment of a variety of diseases, such as respiratory tract infections (59, 60).

One of the genes that is regulated by Upc2 is *ERG11*, a gene involved in ergosterol biosynthesis and the molecular target of the azole antifungals (15, 22, 43, 61, 62). Previous work demonstrated that lower ergosterol levels, caused by ergosterol biosynthesis inhibitors such as azoles, have an inhibitory effect on hyphae formation (63, 64). However, elongated growth forms resulting from impaired Hsp90 function are not considered true hyphae (14, 65, 66). Consistent with the relationship between ergosterol depletion and *C. albicans* morphogenesis mentioned by Victoria *et al.* (67), we report a correlation between ergosterol content and elongated growth caused by impairment of Hsp90 function. The morphogenetic switch to elongated growth forms by either pharmacological inhibition or genetic depletion is accompanied with a significant decrease in ergosterol content. One could question whether this drop in ergosterol is really the cause or rather a consequence of the morphogenetic transition upon Hsp90 inhibition. The formation of elongated growth structures upon low ergosterol levels could be interpreted as a cellular stress response caused by the disruption of the sterol homeostasis. However, this seems unlikely, since our results argue against an elongation-inducing role for low ergosterol levels. First, we demonstrated that reduced levels of Erg11 are not sufficient to promote elongation (Figure 5A). In addition, it was found that increasing concentrations of ascorbic acid reduced ergosterol content without initiating

456 elongated growth (Figure 6A and B). These latter data are consistent with previous
457 observations by Singh *et al.* (68), who reported low ergosterol levels in *C. albicans* cells
458 when they were grown in the presence of ascorbic acid.

459 On the other hand, the increase of ergosterol to wild type levels in the presence of GdA
460 upon addition of ascorbic acid is absent in a *upc2Δ/upc2Δ* mutant suggesting the
461 importance of Upc2 as a transcriptional regulator of Erg11 to overcome the drop in
462 ergosterol levels caused by impaired Hsp90 (Figure 6A). As already mentioned, we show
463 that an increased dosage of *ERG11* alone was not sufficient to overcome the induction of
464 elongated growth upon pharmacological inhibition of Hsp90. This could indicate that
465 ergosterol biosynthesis is not the most important Upc2-mediated effect in response to
466 ascorbic acid or that the expression other *ERG* genes could be regulated by Upc2. We are
467 currently identifying other Upc2-regulated genes by performing ChIP-Seq and RNA-seq
468 analysis. We cannot exclude a possible connection with the previously established
469 pathways in the Hsp90-dependent morphogenetic circuitry, such as the cAMP-PKA and
470 cell cycle pathways or the Pho85-Pcl1-Hms1 module (13, 14, 46, 65, 69) or a novel, yet-
471 to-be-determined pathway. Ascorbic acid or Upc2 may be required for the modulation of
472 an inhibitor of these Hsp90 signalling modules.

473
474 In conclusion, our study elucidates the molecular circuitry through which ascorbic acid
475 influences the Hsp90-dependent *C. albicans* morphogenesis, involving the transcriptional
476 regulator Upc2. We find that ascorbic acid can block the GdA-dependent elongated
477 growth by restoring normal ergosterol levels in a Upc2-dependent fashion. We suggest
478 that influencing ergosterol biosynthesis via Erg11 is not the primary site of action of

Upc2-mediated effects in response to ascorbic acid, as overexpression of *ERG11* did not block elongation upon GdA-treatment. Further research is required to further explore the interesting relationship between Hsp90, Upc2, Erg11 and the morphogenetic machinery.

Acknowledgements

We are grateful to L. Cowen, O. Homann, J. Morschhäuser, D. Sanglard, T. White and T. Roemer for providing strains. We especially thank Ilse Palmans for excellent technical assistance.

This work was supported by an IWT grant from the Flemish Institute for Science and Technology (IWT) to FVH and by the Fund for Scientific Research Flanders (FWO) and the Research Fund of KU Leuven.

References

1. **Blackwell M.** 2011. The fungi: 1, 2, 3 ... 5.1 million species? *Am J Bot* **98**:426-438.
2. **Cheng S-C, Joosten LAB, Kullberg B-J, Netea MG.** 2012. Interplay between *Candida albicans* and the mammalian innate host defense. *Infect Immun* **80**:1304-1313.
3. **Lo HJ, Kohler JR, DiDomenico B, Loebenberg D, Cacciapuoti A, Fink GR.** 1997. Nonfilamentous *C. albicans* mutants are avirulent. *Cell* **90**:939-949.

- 500 4. **Biswas S, Van Dijck P, Datta A.** 2007. Environmental sensing and signal
501 transduction pathways regulating morphopathogenic determinants. *Microbiol.*
502 *Mol. Biol. Rev.* **71**:348-376.
- 503 5. **Pande K, Chen C, Noble SM.** 2013. Passage through the mammalian gut triggers
504 a phenotypic switch that promotes *Candida albicans* commensalism. *Nat Genet*
505 **45**:1088-1091.
- 506 6. **Saville SP, Lazzell AL, Monteagudo C, Lopez-Ribot JL.** 2003. Engineered
507 control of cell morphology in vivo reveals distinct roles for yeast and
508 filamentatous forms of *Candida albicans* during infection. *Eukaryotic Cell*
509 **2**:1053-1060.
- 510 7. **Chandra J, Mukherjee PK, Ghannoum MA.** 2008. *In vitro* growth and analysis
511 of *Candida* biofilms. *Nat Protoc* **3**:1909-1924.
- 512 8. **Sudbery PE, Gow NA, Berman J.** 2004. The distinct morphogenetic states of
513 *Candida albicans*. *Trends Microbiol.* **12**:317-324.
- 514 9. **Albuquerque P, Casadevall A.** 2012. Quorum sensing in fungi - a review. *Med*
515 *Mycol* **50**:337-345.
- 516 10. **Shareck J, Belhumeur P.** 2011. Modulation of morphogenesis in *Candida*
517 *albicans* by various small molecules. *Eukaryot Cell* **10**:1004-1012.
- 518 11. **Hogan DA, Sundstrom P.** 2009. The Ras/cAMP/PKA signaling pathway and
519 virulence in *Candida albicans*. *Future Microbiol* **4**:1263-1270.
- 520 12. **Hogan DA, Muhlschlegel FA.** 2011. *Candida albicans* development regulation:
521 adenylyl cyclase as a coincidence detector of parallel signals. *Curr Opin*
522 *Microbiol* **14**:682-686.

- 523 13. **Shapiro RS, Uppuluri P, Zaas AK, Collins C, Senn H, Perfect JR, Heitman J,**
524 **Cowen LE.** 2009. Hsp90 orchestrates temperature-dependent *Candida albicans*
525 morphogenesis via Ras1-PKA signaling. *Curr Biol* **19**:621-629.
- 526 14. **Shapiro RS, Sellam A, Tebbji F, Whiteway M, Nantel A, Cowen LE.** 2012.
527 Pho85, Pcl1, and Hms1 signaling governs *Candida albicans* morphogenesis
528 induced by high temperature or Hsp90 compromise. *Curr Biol* **22**:461-470.
- 529 15. **MacPherson S, Akache B, Weber S, De Deken X, Raymond M, Turcotte B.**
530 2005. *Candida albicans* zinc cluster protein Upc2p confers resistance to
531 antifungal drugs and is an activator of ergosterol biosynthetic genes. *Antimicrob*
532 *Agents Chemother* **49**:1745-1752.
- 533 16. **Vik A, Rine J.** 2001. Upc2p and Ecm22p, dual regulators of sterol biosynthesis in
534 *Saccharomyces cerevisiae*. *Mol Cell Biol* **21**:6395-6405.
- 535 17. **Znaidi S, Weber S, Al-Abdin OZ, Bomme P, Saidane S, Drouin S, Lemieux S,**
536 **De Deken X, Robert F, Raymond M.** 2008. Genomewide location analysis of
537 *Candida albicans* Upc2p, a regulator of sterol metabolism and azole drug
538 resistance. *Eukaryot Cell* **7**:836-847.
- 539 18. **Heilmann CJ, Schneider S, Barker KS, Rogers PD, Morschhäuser J.** 2010.
540 An A643T mutation in the transcription factor Upc2p causes constitutive *ERG11*
541 upregulation and increased fluconazole resistance in *Candida albicans*.
542 *Antimicrob Agents Chemother* **54**:353-359.
- 543 19. **Hoot SJ, Smith AR, Brown RP, White TC.** 2011. An A643V amino acid
544 substitution in Upc2p contributes to azole resistance in well-characterized clinical
545 isolates of *Candida albicans*. *Antimicrob Agents Chemother* **55**:940-942.

- 546 20. **Flowers SA, Barker KS, Berkow EL, Toner G, Chadwick SG, Gyga SE,**
547 **Morschhäuser J, Rogers PD.** 2012. Gain-of-function mutations in *UPC2* are a
548 frequent cause of *ERG11* upregulation in azole-resistant clinical isolates of
549 *Candida albicans*. Eukaryot Cell **11**:1289-1299.
- 550 21. **Morio F, Pagniez F, Besse M, Gay-andrieu F, Miegville M, Le Pape P.** 2013.
551 Deciphering azole resistance mechanisms with a focus on transcription factor-
552 encoding genes *TAC1*, *MRR1* and *UPC2* in a set of fluconazole-resistant clinical
553 isolates of *Candida albicans*. Int J Antimicrob Agents **42**:410-415.
- 554 22. **Silver PM, Oliver BG, White TC.** 2004. Role of *Candida albicans* transcription
555 factor Upc2p in drug resistance and sterol metabolism. Eukaryot Cell **3**:1391-
556 1397.
- 557 23. **Nasution O, Srinivasa K, Kim M, Kim YJ, Kim W, Jeong W, Choi W.** 2008.
558 Hydrogen peroxide induces hyphal differentiation in *Candida albicans*. Eukaryot
559 Cell **7**:2008-2011.
- 560 24. **Ojha R, Manzoor N, Khan LA.** 2009. Ascorbic acid modulates pathogenicity
561 markers of *Candida albicans*. Internat J Microbiol Res **1**:19-24.
- 562 25. **Eboigbodin KE, Biggs CA.** 2008. Characterization of the extracellular polymeric
563 substances produced by *Escherichia coli* using infrared spectroscopic, proteomic,
564 and aggregation studies. Biomacromolecules **9**:686-695.
- 565 26. **Fu MS, De Sordi L, Muhlschlegel FA.** 2012. Functional characterization of the
566 small heat shock protein Hsp12p from *Candida albicans*. PLoS One **7**:e42894.
- 567 27. **Stynen B, Van Dijck P, Tournu H.** 2010. A CUG codon adapted two-hybrid
568 system for the pathogenic fungus *Candida albicans*. Nucleic Acids Res **38**:e184.

- 569 28. **Care RS, Trevethick J, Binley KM, Sudbery PE.** 1999. The *MET3* promoter: a
570 new tool for *Candida albicans* molecular genetics. *Mol Microbiol* **34**:792-798.
- 571 29. **Arthington-Skaggs BA, Jradi H, Desai T, Morrison CJ.** 1999. Quantification
572 of ergosterol content: novel method for determination of fluconazole
573 susceptibility of *Candida albicans*. *J Clin Microbiol* **37**:3332-3337.
- 574 30. **Odds FC.** 2003. Synergy, antagonism, and what the chequerboard puts between
575 them. *J Antimicrob Chemother* **52**:1.
- 576 31. **Sudbery P.** 2011. Growth of *Candida albicans* hyphae. *Nat Rev Microbiol* **9**:737-
577 748.
- 578 32. **Roe SM, Prodromou C, O'Brien R, Ladbury JE, Piper PW, Pearl LH.** 1999.
579 Structural basis for inhibition of the Hsp90 molecular chaperone by the antitumor
580 antibiotics radicicol and geldanamycin. *J Med Chem* **42**:260-266.
- 581 33. **Homann OR, Dea J, Noble SM, Johnson AD.** 2009. A phenotypic profile of the
582 *Candida albicans* regulatory network. *PLoS Genet* **5**:e1000783.
- 583 34. **Diezmann S, Michaut M, Shapiro RS, Bader GD, Cowen LE.** 2012. Mapping
584 the Hsp90 genetic interaction network in *Candida albicans* reveals environmental
585 contingency and rewired circuitry. *PLoS Genet* **8**:e1002562.
- 586 35. **Schubert S, Barker KS, Znaidi S, Schneider S, Dierolf F, Dunkel N, Aid M,**
587 **Boucher G, Rogers PD, Raymond M, Morschhauser J.** 2011. Regulation of
588 efflux pump expression and drug resistance by the transcription factors Mrr1,
589 Upc2, and Cap1 in *Candida albicans*. *Antimicrob Agents Chemother* **55**:2212-
590 2223.

- 591 36. **Huang Y, Blower PE, Liu R, Dai Z, Pham AN, Moon H, fang J, Sadee W.**
592 2007. Chemogenomic analysis identifies geldanamycins as substrates and
593 inhibitors of ABCB1. *Pharm Res* **24**:1702-1712.
- 594 37. **Workman P.** 2003. Auditing the pharmacological accounts for Hsp90 molecular
595 chaperone inhibitors: unfolding the relationship between pharmacokinetics and
596 pharmacodynamics. *Mol Cancer Ther* **2**:131-138.
- 597 38. **Prasad R, De Wergifosse P, Goffeau A, Balzi E.** 1995. Molecular cloning and
598 characterization of a novel gene of *Candida albicans*, *CDR1*, conferring multiple
599 resistance to drugs and antifungals. *Curr Genet* **27**:320-329.
- 600 39. **Hiller D, Sanglard D, Morschhauser J.** 2006. Overexpression of the MDR1
601 gene is sufficient to confer increased resistance to toxic compounds in *Candida*
602 *albicans*. *Antimicrob Agents Chemother* **50**:1365-1371.
- 603 40. **Dunkel N, Liu TT, Barker KS, Homayouni R, Morschhauser J, Rogers PD.**
604 2008. A gain-of-function mutation in the transcription factor Upc2p causes
605 upregulation of ergosterol biosynthesis genes and increased fluconazole resistance
606 in a clinical *Candida albicans* isolate. *Eukaryot Cell* **7**:1180-1190.
- 607 41. **Becker JM, Kaufman SJ, Hauser M, Huang L, Lin M, Sillaots S, Jian B, Xu**
608 **D, Roemer T.** 2010. Pathway analysis of *Candida albicans* survival and virulence
609 determinants in a murine infection model. *Proc Natl Acad Sci U S A* **107**:22044-
610 22049.
- 611 42. **Fiori A, Van Dijck P.** 2012. Potent synergistic effect of doxycycline with
612 fluconazole against *Candida albicans* is mediated by interference with iron
613 homeostasis. *Antimicrob Agents Chemother* **56**:3785-3796.

- 614 43. **Song JL, Harry JB, Eastman RT, Oliver BG, White TC.** 2004. The *Candida*
615 *albicans* lanosterol 14- α -demethylase (*ERG11*) gene promoter is maximally
616 induced after prolonged growth with antifungal drugs. Antimicrob Agents
617 Chemother **48**:1136-1144.
- 618 44. **Dhamgaye S, Devaux F, Manoharlal R, Vandeputte P, Shah AH, Singh A,**
619 **Blugeon D, Sanglard D, Prasad R.** 2012. In vitro effect of malachite green on
620 *Candida albicans* involves multiple pathways and transcriptional regulators
621 *UPC2* and *STP2*. Antimicrob Agents Chemother **56**:495-506.
- 622 45. **Wang Y, Jia XM, Jia JH, Li MB, Cao YY, Gao PH, Liao WQ, Cao YB, Jiang**
623 **YY.** 2009. Ascorbic acid decreases the antifungal effect of fluconazole in the
624 treatment of candidiasis. Clin Exp Pharmacol Physiol **36**:e40-46.
- 625 46. **Shapiro RS, Zaas AK, Betancourt-Quiroz M, Perfect JR, Cowen LE.** 2012.
626 The Hsp90 co-chaperone Sgt1 governs *Candida albicans* morphogenesis and drug
627 resistance. PLoS One **7**:e44734.
- 628 47. **Shapiro RS, Cowen LE.** 2012. Thermal control of microbial development and
629 virulence: molecular mechanisms of microbial temperature sensing. MBio
630 **3**:e00238-00212.
- 631 48. **Dikalov S, Landmesser U, Harrison DG.** 2002. Geldanamycin leads to
632 superoxide formation by enzymatic and non-enzymatic redox cycling.
633 Implications for studies of Hsp90 and endothelial cell nitric-oxide synthase. J Biol
634 Chem **277**:25480-25485.
- 635 49. **Deneke SM.** 2000. Thiol-based antioxidants. Curr Top Cell Regul **36**:151-180.

- 636 50. **Patterson MJ, McKenzie CG, Smith DA, da Silva Dantas A, Sherston S, Veal**
637 **EA, Morgan BA, MacCallum DM, Erwig LP, Quinn J.** 2013. Ybp1 and Gpx3
638 signaling in *Candida albicans* govern hydrogen-peroxide-induced oxidation of the
639 Cap1 transcription factor and macrophage escape. *Antioxid Redox Signal*
640 **19:2244-2260.**
- 641 51. **Huh WK, Kim ST, Kim H, Jeong G, Kang SO.** 2001. Deficiency of D-
642 erythroascorbic acid attenuates hyphal growth and virulence of *Candida albicans*.
643 *Infect Immun* **69:3939-3946.**
- 644 52. **Moulin E, Zoete V, Barluenga S, Karplus M, Winssinger N.** 2005. Design,
645 synthesis, and biological evaluation of HSP90 inhibitors based on conformational
646 analysis of radicicol and its analogues. *J Am Chem Soc* **127:6999-7004.**
- 647 53. **Cysyk RL, Parker RJ, Barchi Jr JJ, Steeg PS, Hartman NR, Strong JM.**
648 2006. Reaction of geldanamycin and C17-substituted analogues with glutathione:
649 product identifications and pharmacological implications. *Chem Res Toxicol*
650 **19:376-381.**
- 651 54. **Guo W, Reigan P, Siegel D, Ross D.** 2008. Enzymatic reduction and glutathione
652 conjugation of benzoquinone ansamycin heat shock protein 90 inhibitors:
653 relevance for toxicity and mechanism of action. *Drug Metab Dispos* **36:2050-**
654 **2057.**
- 655 55. **Samuni A, Goldstein S.** 2012. Redox properties and thiol reactivity of
656 geldanamycin and its analogues in aqueous solutions. *J Phys Chem B* **116:6404-**
657 **6410.**

- 658 56. **Ross D.** 1988. Glutathione, free radicals and chemotherapeutic agents.
659 Mechanisms of free-radical induced toxicity and glutathione-dependent
660 protection. *Pharmacol Therapeut* **37**:231-249.
- 661 57. **Agatsuma T, Ogawa H, Akasaka K, Asai A, Yamashita Y, Mizukami T,**
662 **Akinaga S, Saitoh Y.** 2002. Holydrin and oxime derivatives of radicicol:
663 synthesis and antitumor activities. *Bioorg Med Chem* **10**:2445-3454.
- 664 58. **Padayatty SJ, Katz A, Wang Y, Eck P, Kwon O, Lee JH, Chen S, Corpe C,**
665 **Dutta A, Dutta SK, Levine M.** 2003. Vitamin C as an antioxidant: evaluation of
666 its role in disease prevention. *J Am Coll Nutr* **22**:18-35.
- 667 59. **Arrol B.** 2005. Non-antibiotic treatments for upper-respiratory tract infections
668 (common cold). *Respir Med* **99**:1477-1484.
- 669 60. **Stephensen CB, Marquis GS, Jacob RA, Kruzich LA, Douglas SD, Wilson**
670 **CM.** 2006. Vitamins C and E in adolescents and young adults with HIV infection.
671 *Am J Clin Nutr* **83**:870-879.
- 672 61. **Oliver BG, Song JL, Choiniere JH, White TC.** 2007. cis-Acting elements
673 within the *Candida albicans* *ERG11* promoter mediate the azole response through
674 transcription factor Upc2p. *Eukaryot Cell* **6**:2231-2239.
- 675 62. **Hoot SJ, Oliver BG, White TC.** 2008. *Candida albicans* *UPC2* is
676 transcriptionally induced in response to antifungal drugs and anaerobicity through
677 Upc2p-dependent and -independent mechanisms. *Microbiol* **154**:2748-2756.
- 678 63. **Ha KC, White TC.** 1999. Effects of azole antifungal drugs on the transition from
679 yeast cells to hyphae in susceptible and resistant isolates of the pathogenic yeast
680 *Candida albicans*. *Antimicrob Agents Chemother* **43**:763-768.

- 681 64. **Odds FC, Cockayne A, Hayward J, Abbott AB.** 1985. Effects of imidazole-
682 and triazole-derivative antifungal compounds on the growth and morphological
683 development of *Candida albicans* hyphae. J Gen Microbiol **131**:2581-2589.
- 684 65. **Senn H, Shapiro RS, Cowen LE.** 2012. Cdc28 provides a molecular link
685 between Hsp90, morphogenesis, and cell cycle progression in *Candida albicans*.
686 Mol Biol Cell **23**:268-283.
- 687 66. **Bachewich C, Nantel A, Whiteway M.** 2005. Cell cycle arrest during S or M
688 phase generates polarized growth via distinct signals in *Candida albicans*. Mol.
689 Microbiol. **57**:942-959.
- 690 67. **Victoria GS, Yadav B, Lauhnar L, Jain P, Bhatnagar S, Komath SS.** 2012.
691 Mutual co-regulation between GPI-N-acetylglucosaminyltransferase and
692 ergosterol biosynthesis in *Candida albicans*. Biochem J **443**:619-625.
- 693 68. **Singh M, Jayakumar A, Prasad R.** 1979. The effect of altered ergosterol
694 content on the transport of various amino acids in *Candida albicans*. Biochim
695 Biophys Acta **555**:42-55.
- 696 69. **Serneels J, Tournu H, Van Dijck P.** 2012. Tight control of trehalose content is
697 required for efficient heat-induced cell elongation in *Candida albicans*. J Biol
698 Chem **287**:36873-36882.
- 699 70. **Gillum AM, Tsay EYH, Kirsch DR.** 1984. Isolation of the *Candida albicans*
700 gene for orotidine-5'-phosphate decarboxylase by complementation of *S.*
701 *cerevisiae* *ura3* and *E. coli* *pyrF* mutations. Mol Gen Genet **198**:179-182.
- 702 71. **Fonzi WA, Irwin MY.** 1993. Isogenic strain construction and gene mapping in
703 *Candida albicans*. Genetics **134**:717-728.

- 704 72. **Sanglard D, Ischer F, Monod M, Bille J.** 1996. Susceptibilities of *Candida*
705 *albicans* multidrug transporter mutants to various antifungal agents and other
706 metabolic inhibitors. *Antimicrob Agents Chemother* **40**:2300-2305.
- 707 73. **Noble SM, Johnson AD.** 2005. Strains and strategies for large-scale gene
708 deletion studies of the diploid human fungal pathogen *Candida albicans*.
709 *Eukaryot. Cell* **4**:298-309.
- 710 74. **Cowen LE, Singh SD, Kohler JR, Collins C, Zaas AK, Schell WA, Aziz H,**
711 **Mylonakis E, Perfect JR, Whitesell L, Lindquist S.** 2009. Harnessing Hsp90
712 function as a powerful, broadly effective therapeutic strategy for fungal infectious
713 disease. *Proc Natl Acad Sci U S A* **106**:2818-2823.
- 714
- 715
- 716
- 717

Figure legends

Figure 1: Ascorbic acid abrogates GdA-induced elongated growth

A) Inhibiting effect of ascorbic acid on elongated growth induced by 10 μ M GdA. Wild type SC5314 cells were grown at 30 °C in liquid rich medium containing GdA (10 μ M) with 2.5 mM ascorbic acid. Pictures were taken after 8 h of growth. B) GdA-mediated pharmacological inhibition of Hsp90 for extended periods of times is not lethal. Propidium Iodide stained heat-killed wild type cells (15 min at 80 °C) are clearly illustrating a complete lethal phenotype as indicated by the staining (which is excluded from viable cells), while the GdA-treated cells closely resemble the untreated wild type cells. Pictures were taken after 24 h.

Figure 2: Ascorbic acid influences phenotypes caused by Hsp90 genetic depletion

A) Ascorbic acid (2.5 mM) counteracts elongated growth upon genetic depletion of Hsp90 (0.1 μ g/ml Dox). Pictures were taken after 24 h. B) Genetic depletion of Hsp90 for extended of times in the periods of times in the presence of 0.1 μ g/ml doxycycline is not completely lethal. Propidium iodide stained heat killed wild type cells (15 min at 80 °C) are clearly illustrating a complete lethal phenotype as indicated by the staining, while the cells genetically depleted of Hsp90 closely resemble the untreated wild type cells. Pictures were taken at 24 h. C) The percentage of yeast cells grown for 24 h in the presence of ascorbic acid was significantly (**p < 0.001) higher compared to the untreated condition D) The sedimentation rate was monitored of cultures of a *Candida* strain in which the remaining *Hsp90* was under control of a tetracycline-repressible

promoter in liquid YPD rich medium supplemented with 0.1 µg/ml Dox (■), 0.1 µg/ml Dox + 2.5 mM L-Cysteine (◇), 0.1 µg/ml Dox + 2.5 mM ascorbic acid (▲) and 0.1 µg/ml Dox + 2.5 mM Glutathione (●). The graphs were plotted by percentage of cells sedimented against time.

Figure 3: Overexpression of *UPC2* represses GdA-induced elongated growth

A) Quantitative real-time PCR of *UPC2* expression under the control of the inducible *MET3* promoter, in the *UPC2* overexpression strain and the control strain carrying an identical construct with the exception of the transcription factor. Promoter repressing conditions in the presence of 10 mM methionine are represented in white, while the black bars represent inducing conditions. The graph shows mean values with standard deviations from two independent experiments. B) The inducible *MET3* promoter allows regulated expression. Overexpression of *UPC2* in the presence of GdA (10 µM) blocks the rise of the characteristic elongated growth form. This yeast form is reversed to the elongated structures under promoter repressing conditions (represented by addition of 10 mM methionine). The control strain carrying an identical expression construct except the transcriptional regulator, displays a filamentous growth form in both promoter repressing and inducing conditions. Pictures were taken after 8 h of growth at 30 °C in CSM-met medium.

Figure 4: The *UPC2* deletion strain is hypersusceptible for GdA and impairs ascorbic acid associated blockage of the elongated cell shape

A. The *UPC2* deletion strain is hypersusceptible to GdA. The *upc2Δ/upc2Δ* (D-6) strain was tested for its hypersusceptibility to GdA by treating them with 4 μM of GdA, a concentration that is unable to induce elongated growth in the corresponding wild type. The *UPC2* re-integrant strain (EC-7) displays a similar phenotype as the wild type. Pictures were taken after 8 h of growth at 30 °C in YPD medium. B. Deletion of *UPC2* impairs ascorbic acid associated blockage of the elongated cell shape. Deletion strains were grown at 30 °C in YPD rich medium supplemented with either 10 μM GdA, 2.5 mM L-ascorbic acid or a combination of both. While ascorbic acid blocks the GdA-induced filamentation of the wild-type strain, it is unable to do so in the *upc2Δ/upc2Δ* mutants D-6 and TF077, while the reconstitution of *UPC2* restores the yeast growth response. Pictures were taken after 8 h.

Figure 5: *ERG11* is required for the ascorbic acid-mediated effect

A) A *tetO-ERG11/erg11Δ* was grown at 30 °C in YPD rich medium supplemented with either 10 μM GdA, 2.5 mM L-ascorbic acid, 0.1 μg/ml doxycycline or a combination of these substances. While ascorbic acid blocks elongation upon GdA-treatment of the *tetO-ERG11/erg11Δ* in the absence of doxycycline, compromising *ERG11* expression is able to overcome this ascorbic acid associated blockage. Pictures were taken after 8 h. B) Overexpression of *ERG11* is not sufficient to block elongated growth caused by Hsp90 inhibition. *C. albicans* strains AFA60 (control) and AFA59b (*ACT1p-CaERG11*) were grown at 30 °C in YPD rich medium supplemented with 10μM GdA. GdA-induced elongation of both the control and the *ACT1p-CaERG11* strain shows that an increased

dosage of Erg11 cannot suppress elongation. Pictures were taken after 8 h. C) There is a significant drop ($*p < 0.05$) in *ERG11* expression upon GdA treatment in the wild type, while simultaneous addition of ascorbic acid upon this treatment leads to an increase. Interestingly, this latter observation is absent in the *upc2Δ/upc2Δ* mutant, suggesting a role for Upc2. Data are means of \pm standard deviations of triplicate experiments.

Figure 6: Hsp90 inhibition or depletion result in reduced intracellular ergosterol levels

A) Ergosterol measurements in the wild type and *upc2Δ/upc2Δ* mutant show a significant decrease in ergosterol content after pharmacological inhibition of Hsp90 in comparison with the representative untreated control ($*p < 0.05$; $**p < 0.001$). Addition of ascorbic acid under these conditions was reflected by an increase of ergosterol content only in the wild type. Results are means of at least three independent measurements. Legend: Black: untreated; Dark grey: 2.5 mM ascorbic acid; Light grey: 10 μ M GdA; White: 10 μ M GdA + 2.5 mM ascorbic acid. Data are means of \pm standard deviations of triplicate experiments.

B) Ergosterol measurements in the *tetO- HSP90/hsp90Δ* strain show a similar significant decrease in ergosterol content in the presence of doxycycline (0.1 μ g/ml) compared to the untreated control ($*p < 0.05$; $**p < 0.001$). This drop in ergosterol levels has great similarities with pharmacological inhibition by GdA. Addition of ascorbic acid is reflected by an increase in ergosterol content in the presence of doxycycline, while there is a general decrease noticeable in its absence. Data are means of \pm standard deviations of triplicate experiments.

Tables

Table 1 : Strains used in this study

Strain	Description	Genotype	Source
SC5314		Wild type	(70)
CAI4		<i>ura3Δ::imm434/ura3Δ::imm434</i> <i>iro1Δ/iro1Δ::imm343</i>	(71)
AFA60a	CAI4 transformed with <i>URA3</i> vector	<i>ura3Δ::imm434/ura3Δ::imm434</i> <i>iro1Δ/iro1Δ::imm343 RPS10::CIP10</i>	(42)
AFA59b	CAI4 carrying extra copy of <i>CaERG11</i> under control of <i>ACT1</i> promoter	<i>ura3Δ::imm434/ura3Δ::imm434</i> <i>iro1Δ/iro1Δ::imm343</i> <i>RPS10::pAFC89b</i>	(42)
DSY448	<i>cdr1Δ/cdr1Δ</i> mutant	<i>ura3Δ::imm434/ura3Δ::imm434</i> <i>iro1Δ/iro1Δ::imm343 cdr1Δ::hisG-URA3-hisG/cdr1Δ::hisG</i>	(72)
DSY465	<i>mdr1Δ/mdr1Δ</i> mutant	<i>ura3Δ::imm434/ura3Δ::imm434</i> <i>iro1Δ/iro1Δ::imm343 benΔ::hisG-URA3-hisG/benΔ::hisG</i>	(72)
CMDR1E2 A and -B	CAI4 carrying <i>CaMDR1</i> under control of <i>ADH1</i> promoter	<i>ura3Δ::imm434/ura3Δ::imm434</i> <i>iro1Δ/iro1Δ::imm343</i> <i>ADH1/adh1::P_{ADH1}-MDR1-URA3</i>	(39)
SN152	Background strain TF wild type and TF077	<i>arg4Δ/arg4Δ leu2Δ /leu2Δ</i> <i>his1Δ/his1Δ URA3/ura3Δ::imm434</i> <i>IRO1/iro1Δ::imm343</i>	(73)
TF wild type	Control wild type strain (paired “wild type” TF077)	<i>arg4Δ /arg4Δ leu2Δ /LEU2</i> <i>his1Δ/HIS1 URA3/ura3Δ::imm434</i> <i>IRO1/iro1Δ::imm343</i>	(33)

TF077	<i>upc2Δ/upc2Δ</i> mutant	As SN152, but <i>upc2Δ::HIS1/upc2Δ::LEU2</i>	(33)
BWP17 (TW14901)	Background strain D-6 and EC-7	<i>ura3Δ::imm434/ura3Δ::imm434</i> <i>iro1/iro1Δ::imm434</i> <i>his1Δ::hisG/his1Δ::hisG</i> <i>arg4Δ/arg4Δ</i>	(22)
D-6 (TW14903)	<i>upc2Δ/upc2Δ</i> mutant	As BWP17 but <i>upc2Δ::URA3/upc2Δ::ARG4</i>	(22)
EC-7 (TW14904)	Reconstituted strain	As D-6 but <i>upc2Δ::URA3/upc2Δ::UPC2-HIS1</i>	(22)
<i>pTET-ERG11</i>	CAI4 with doxycycline-repressible <i>ERG11</i> as the only <i>ERG11</i> allele	As CAI4, but <i>tetO-ERG11/erg11Δ</i>	(41)
CaLC1411 (CaLC436)	Strain with doxycycline-repressible <i>HSP90</i> as the only <i>HSP90</i> allele	<i>arg4Δ/arg4Δhis1Δ/his1ΔURA3/ura3Δ::imm434 IRO1/iro1Δ::imm434</i> <i>HIS1/his1Δ::TAR-FRT</i> <i>hsp90Δ::CdHIS1/his1Δ::TAR-FRT</i>	(74)
SC2H3		As SN152, but 5xLexAOp-ADH1b/HIS1 5xLexAOp-ADH1b/lacZ	(27)
OX Control	Strain carrying empty vector under <i>MET3</i> promoter	As SC2H3, but <i>MET3pro:lexA</i>	Stynen <i>et al.</i> , under preparation
Upc2 OX	Strain carrying extra copy of <i>UPC2</i> under <i>MET3</i> promoter	As SC2H3, but <i>MET3pro:lexA:UPC2</i>	Stynen <i>et al.</i> , under preparation
Gcn4 OX	Strain carrying extra copy of	As SC2H3, but	Stynen <i>et</i>

	<i>GCN4</i> under <i>MET3</i> promoter	<i>MET3pro:lexA:GCN4</i>	<i>al.</i> , under preparation
Cap1 OX	Strain carrying extra copy of <i>CAP1</i> under <i>MET3</i> promoter	As SC2H3, but <i>MET3pro:lexA:CAP1</i>	Stynen <i>et al.</i> , under preparation
Dot6 OX	Strain carrying extra copy of <i>DOT6</i> under <i>MET3</i> promoter	As SC2H3, but <i>MET3pro:lexA:DOT6</i>	Stynen <i>et al.</i> , under preparation
Rtg3 OX	Strain carrying extra copy of <i>RTG3</i> under <i>MET3</i> promoter	As SC2H3, but <i>MET3pro:lexA:RTG3</i>	Stynen <i>et al.</i> , under preparation

Table 2: Primers used in this study

Primer	Description	Source
CaERG11 up	TTACCTCATTATTGGAGACGTGATG	(42)
CaERG11 down	CACGTTCTCTTCTCAGTTTAATTTCTTTC	(42)
TEF1a_fw	CCACTGAAGTCAAGTCCGTTGA	(42)
TEF1a-rv	CACCTTCAGCCAATTGTTCTGT	(42)
UPC2_fw	GGATGCTCGACATGCAAAAAG	This study
UPC2_rv	TGCCACATACAGGTCTCTGTTCA	This study
HSP90_fw	CCATCTGATATCACTCAAGATG	This study
HSP90_rv	AGTGATAAACACTCTACGGACG	This study

818

819 **Table 3: Transcription factors that upon overexpression block the GdA-induced elongated growth.**

Upc2	Zn ₂ -Cys ₆ transcriptional regulator of ergosterol biosynthetic genes and sterol uptake
Cap1	AP-1 family bZIP transcription factor involved in drug resistance and oxidative stress regulation
Dot6	Uncharacterized ORF, protein with a predicted role in telomeric gene silencing and filamentation
Rtg3	Uncharacterized ORF, putative transcription factor with bZIP DNA-binding motif
Gcn4	bZIP transcription factor involved in amino acid control response

820

821

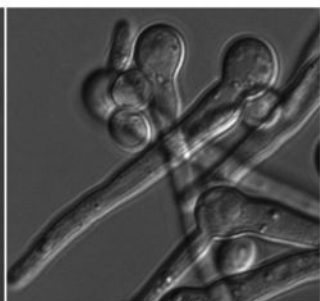
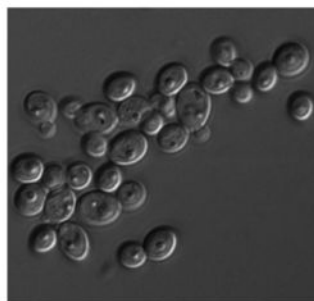
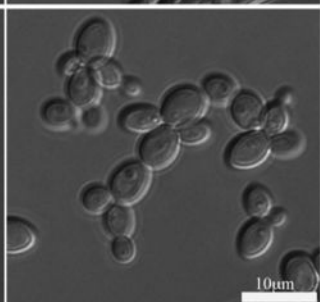
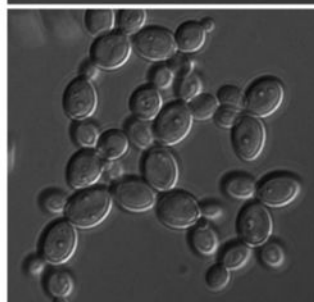
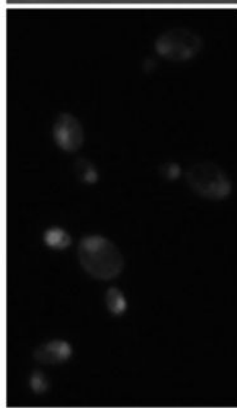
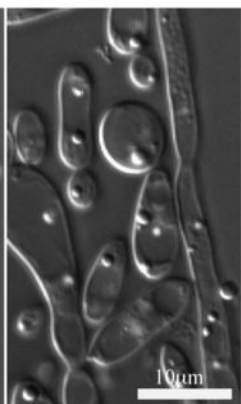
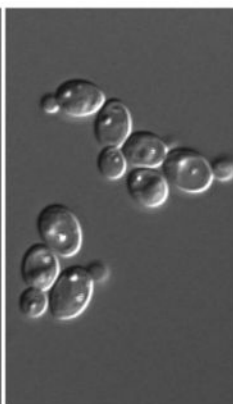
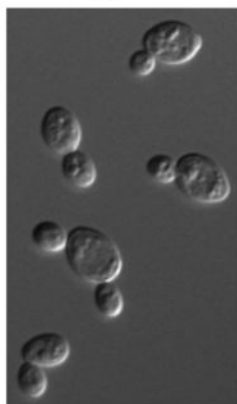
822 **Table 4: The antagonistic effect of ascorbic acid on fluconazole is not present in a *upc2Δ/upc2Δ***
823 **mutant.** MIC_{FLC} and MIC_{AA} are MICs of fluconazole and ascorbic alone, while MIC_{FLC/AA} and MIC_{AA/FLC}
824 are MICs of ascorbic acid and fluconazole in combination. Interpretation of the FIC index was performed
825 as previously described (30).

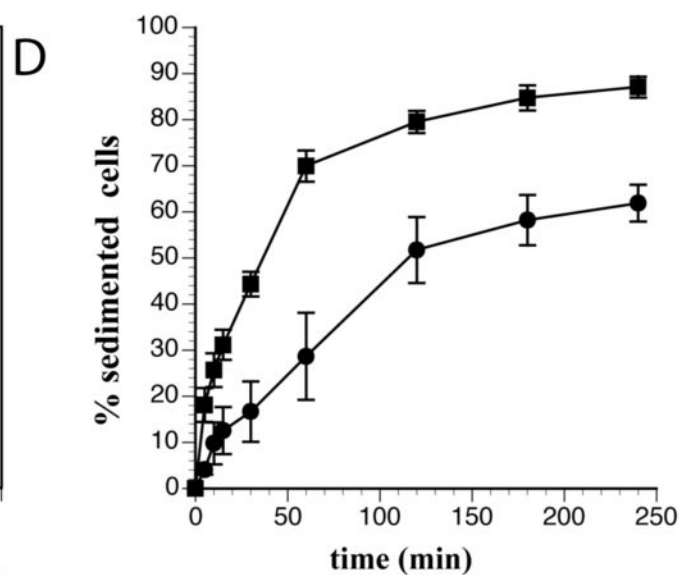
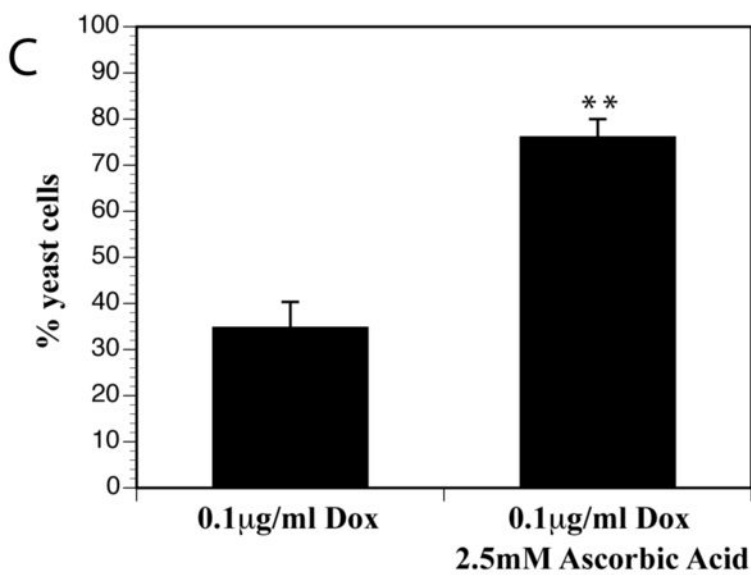
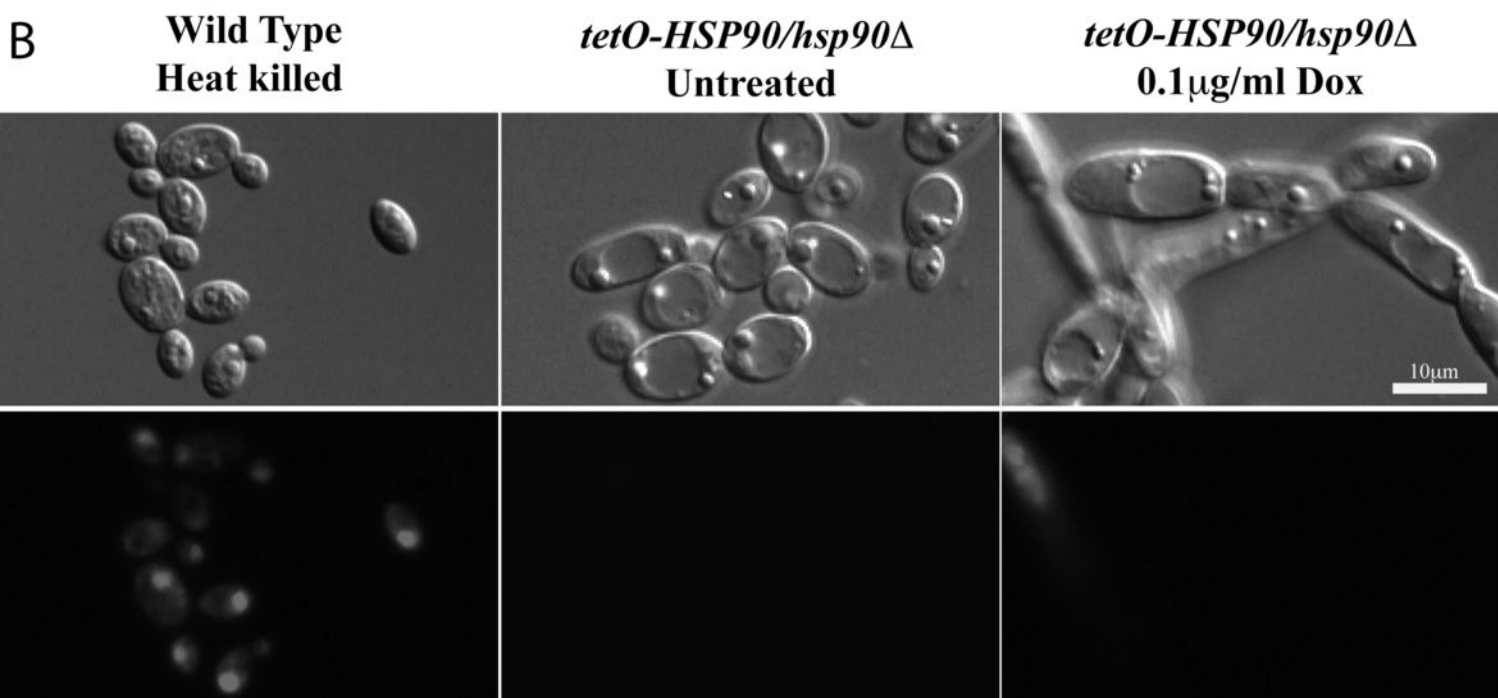
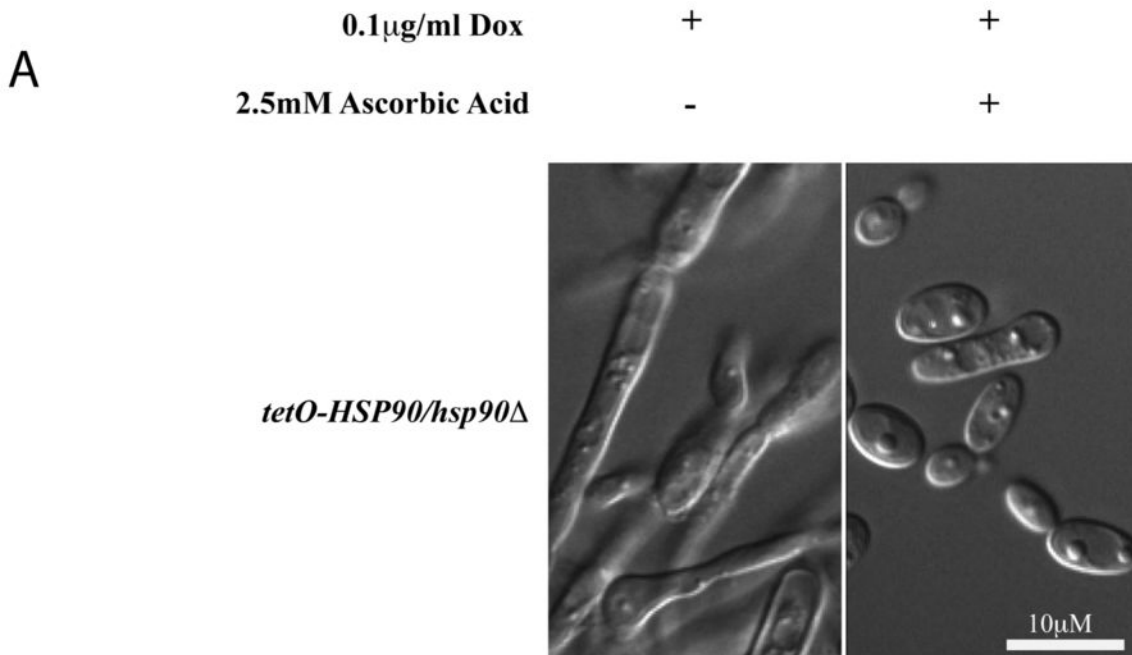
Strain	MIC _{FLC}	MIC _{FLC/AA}	MIC _{AA}	MIC _{AA/FLC}	FIC index
Wild type	2 µg/ml	>64 µg/ml	1761.2 µg/ml (10 mM)	1761.2 µg/ml (10 mM)	33
<i>upc2Δ/upc2Δ</i>	0.25 µg/ml	0.125 µg/ml	1761.2 µg/ml (10 mM)	440.3 µg/ml (2.5 mM)	0.75

826

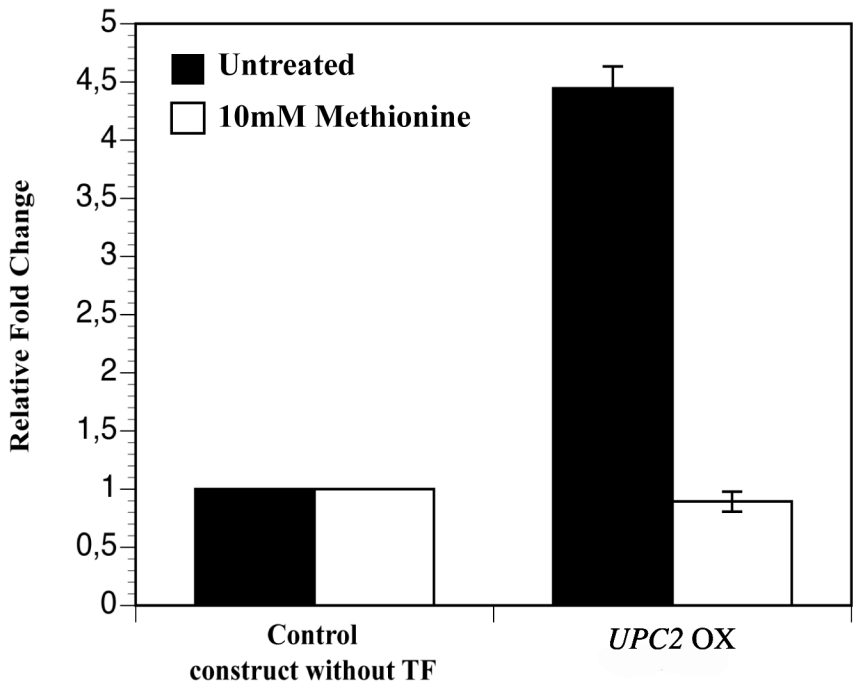
827

828

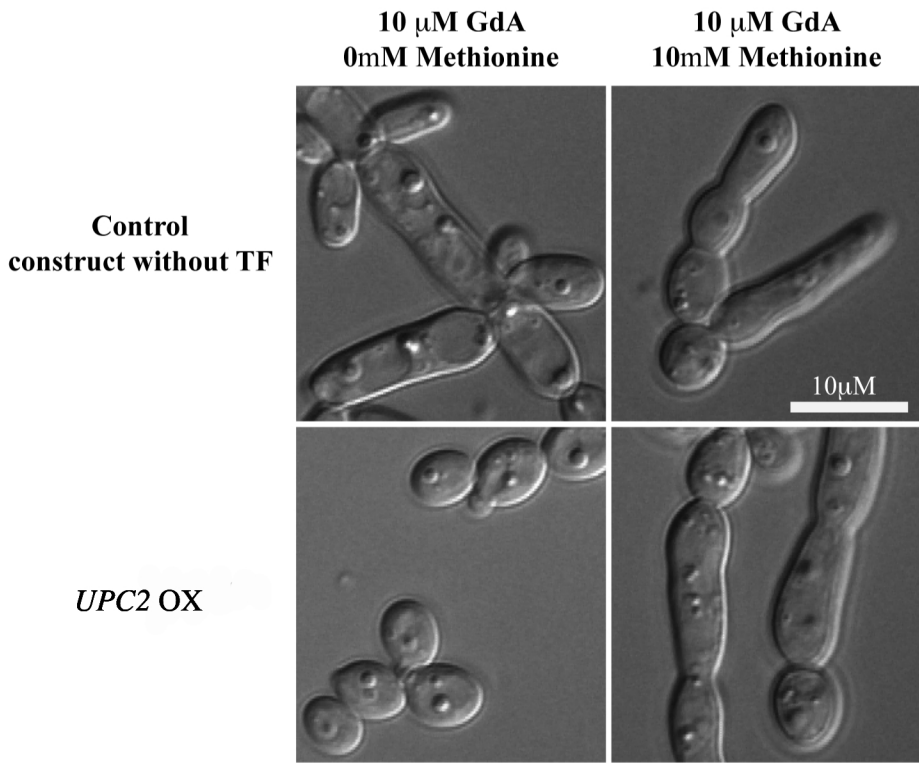
A**- GdA****10 μ M GdA****Untreated****2.5 mM Ascorbic acid****B****Heat killed
Wild type control****Wild type
Untreated****Wild type
10 μ M GdA**



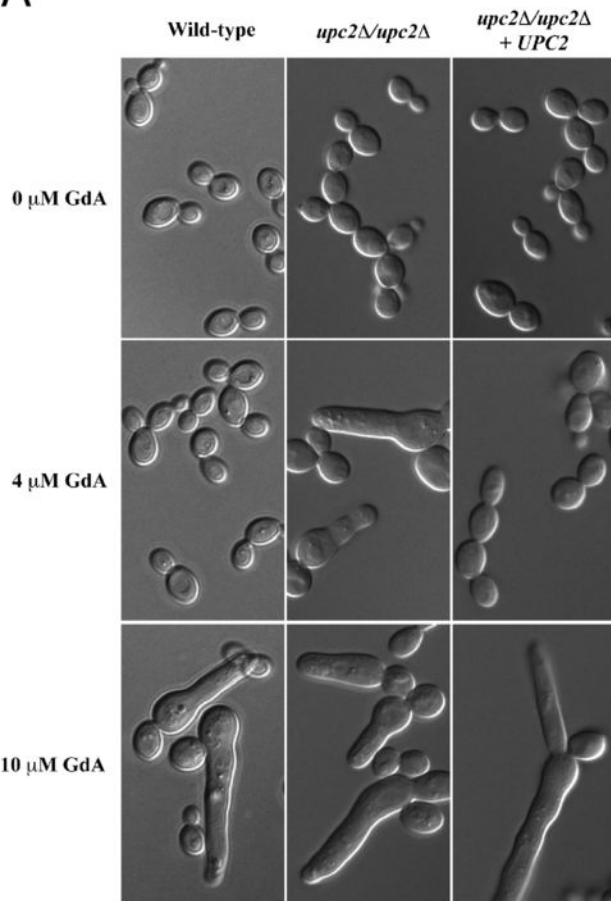
A



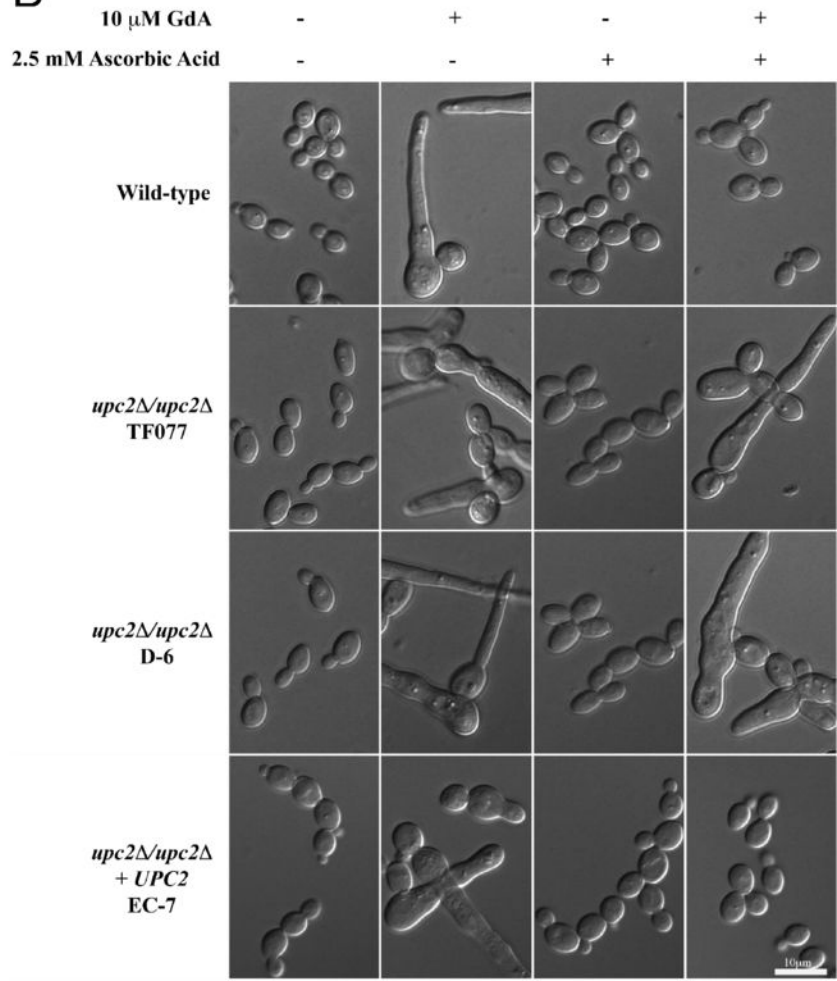
B



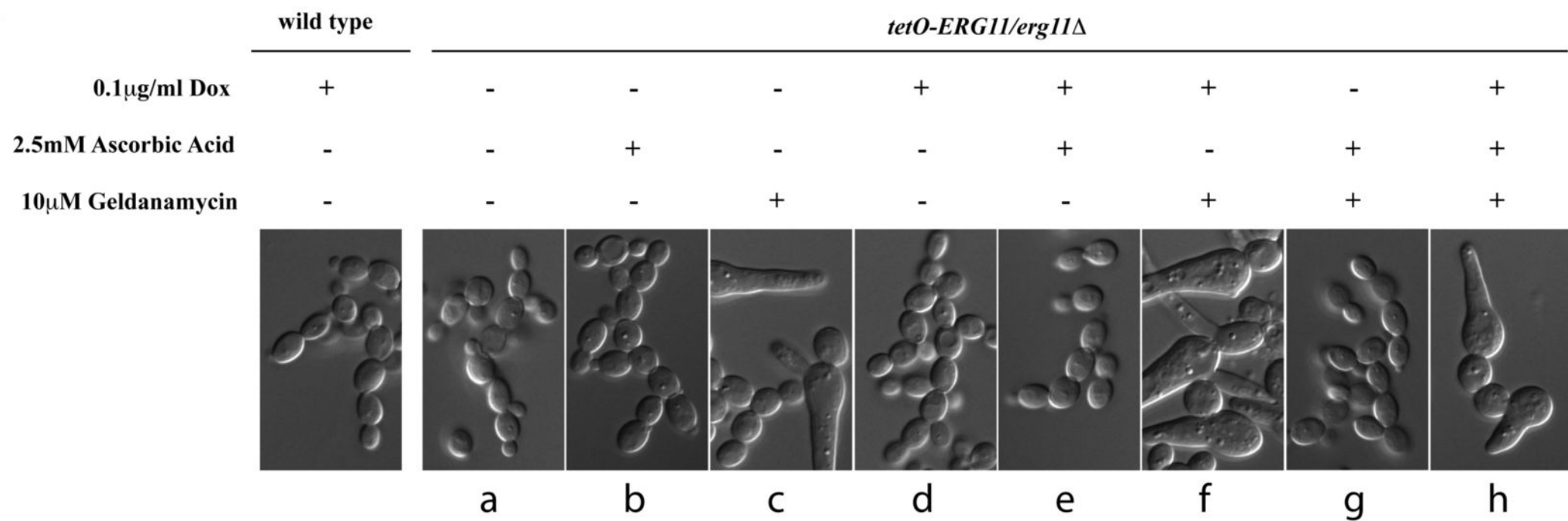
A



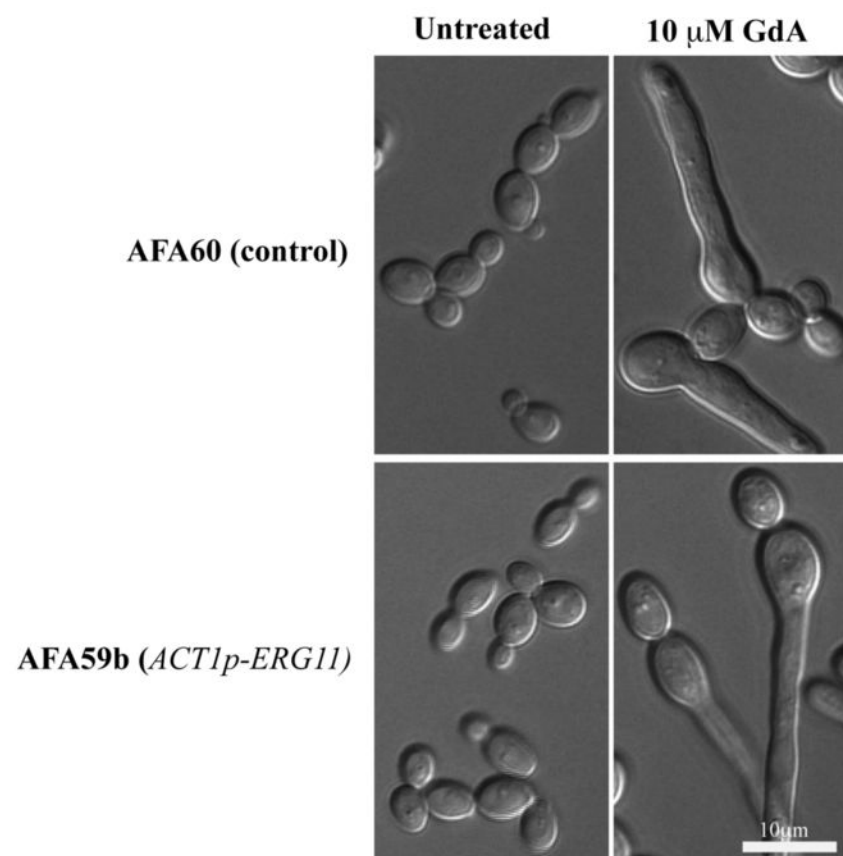
B



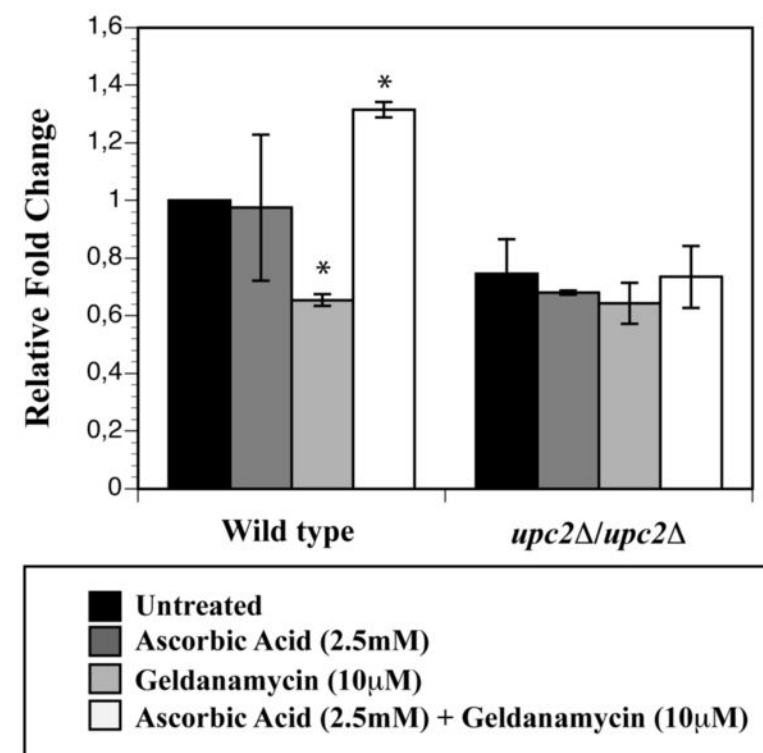
A



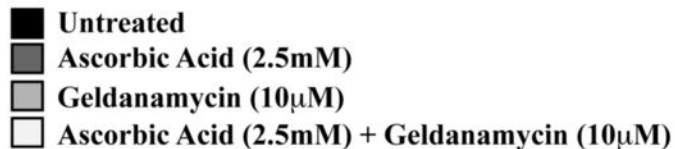
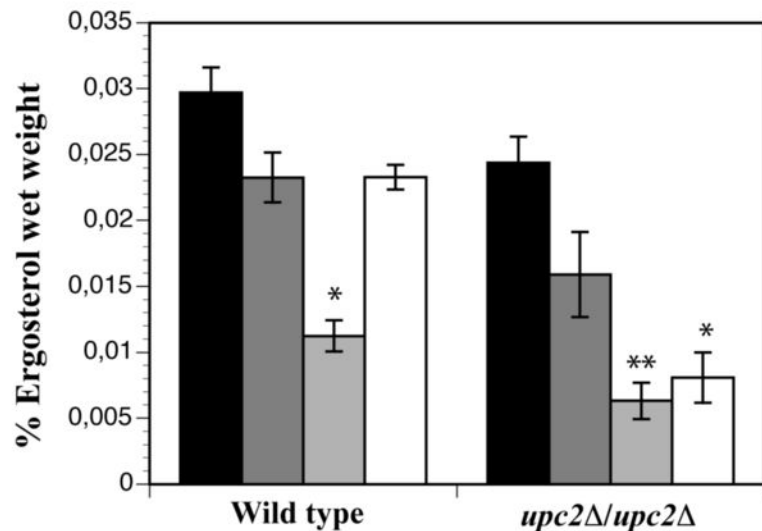
B



C



A



B

